

GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: August 9, 2002, 20:03:32 ; Search time 24.96 Seconds  
(without alignments)  
720.812 Million cell updates/sec

Title: US-09-622-613a-2  
Perfect score: 576  
Sequence: 1 ODWLTFQKKHLNTRDVCN.....TFCVTCENQAPVHVGVC 104

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues

Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database : Listing first 45 summaries

SPTREMBL\_19:\*  
1: sp.archaea:\*  
2: sp.bacteria:\*  
3: sp.fungi:\*  
4: sp.human:\*  
5: sp.invertebrate:\*  
6: sp.mammal:\*  
7: sp.mhc:\*  
8: sp.organelle:\*  
9: sp.phage:\*  
10: sp.plant:\*  
11: sp.podent:\*  
12: sp.virus:\*  
13: sp.vertbrate:\*  
14: sp.unclassified:\*  
15: sp.virus:\*  
16: sp.bacteriap:\*  
17: sp.archaeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	569	98.8	127	13	Q918V8
2	395.5	68.7	129	13	Q9DFV6
3	387	67.2	128	13	Q9DFY8
4	317	55.0	128	13	Q9DFY7
5	315	54.7	128	13	Q9DFY5
6	297	51.6	133	13	Q98SM0
7	291	50.5	133	13	Q9PWR7
8	284	49.3	132	13	Q98SM2
9	279	48.4	132	13	Q98SM1
10	277	48.1	133	13	Q98SL9
11	274.5	47.7	132	13	Q9DF78
12	273	47.4	133	13	Q98SL8
13	153.5	26.6	169	13	Q9W738
14	135	23.4	152	11	Q9JK15
15	129	22.4	154	11	Q9JK18
16	128	22.2	157	11	Q9JK19

17	127	22.0	157	11	Q9JKJ3	Q9JKJ3 meriones un
18	126.5	22.0	155	11	Q9JKH9	Q9JKH9 mus pahari
19	126	21.9	157	11	Q9JKJ4	Q9JKJ4 meriones un
20	124	21.5	148	6	Q9GKP9	Q9GKP9 bos taurus
21	123	21.4	157	11	Q9JKJ1	Q9JKJ1 meriones un
22	122.5	21.3	132	6	Q9TV25	Q9TV25 eulemur ful
23	122	21.2	157	11	Q9JKJ2	Q9JKJ2 meriones un
24	121.5	21.1	155	11	Q9JKJ4	Q9JKJ4 mus saxicol
25	119.5	20.7	170	6	Q9BEC1	Q9BEC1 tragulus ja
26	118.5	20.6	119	6	Q9TV32	Q9TV32 gorilla gor
27	118.5	20.6	153	11	Q9JKI7	Q9JKI7 mus saxicol
28	118	20.5	156	11	Q9JKG6	Q9JKG6 mus caroli
29	117.5	20.4	155	11	Q9RI25	Q9RI25 mus musculu
30	117.5	20.4	155	11	Q9JKG7	Q9JKG7 mus caroli
31	117	20.3	156	11	Q9JKG7	Q9JKG7 mus caroli
32	116.5	20.2	119	6	Q9TS06	Q9TS06 ceropithec
33	116.5	20.2	155	11	Q9JKH8	Q9JKH8 mus pahari
34	116	20.1	156	11	Q9JKH7	Q9JKH7 mus caroli
35	116	20.1	156	11	Q9JKH5	Q9JKH5 mus caroli
36	116	20.1	156	11	Q9JKH4	Q9JKH4 mus caroli
37	116	20.1	156	11	Q9JKG9	Q9JKG9 mus caroli
38	115.5	20.1	155	11	Q9JKI6	Q9JKI6 mus saxicol
39	113	19.6	116	6	Q9TVC0	Q9TVC0 sus scrofa
40	113	19.6	156	11	Q923L6	Q923L6 mus musculu
41	112.5	19.5	132	6	Q9TV24	Q9TV24 galago moho
42	112	19.4	145	6	Q95J16	Q95J16 pan troglod
43	112	19.4	156	11	Q9JKH2	Q9JKH2 mus caroli
44	112	19.4	156	11	Q9JKH1	Q9JKH1 mus caroli
45	111.5	19.4	119	6	Q9TV31	Q9TV31 salmali sal

## ALIGNMENTS

RESULT	ID	1	PRELIMINARY:	PRT:	127 AA.
Q918V8	Q918V8				
AC	Q918V8:				
DT	01-OCT-2000 (TREMBLREL. 15, Created)				
DT	01-OCT-2000 (TREMBLREL. 15, Last sequence update)				
DT	01-DEC-2001 (TREMBLREL. 19, Last annotation update)				
DE	ONCONASE VARIANT RAPRI PRECURSOR.				
OS	Rana pipiens (Northern leopard frog).				
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;				
CC	Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Rana.				
OX	NCBI_TaxID=8404;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	TISSUE=LIVER:				
RX	MEDLINE=20330357; PubMed=10871370;				
RA	Chen S.-L., Le S.-Y., Newton D.L., Maizel J.V. Jr., Rybak S.M.;				
RT	"A gender-specific mRNA encoding a cytotoxic ribonuclease contains a				
RT	3' UTR of unusual length and structure."				
RL	Nucleic Acids Res. 28:2375-2382(2000).				
DR	EMBL; AF165133; AAF76935.1; -				
DR	HSSP; P22069; IONC				
DR	InterPro; IPR001427; RNaseA.				
DR	Pfam; PF00074; fnasea; 1.				
DR	ProDom; PD000535; RNaseA; 1.				
DR	SMART; SM00092; RNase_Pc; 1.				
DR	PROSITE; PS00127; RNASE_PANCREATIC; UNKNOWN_1.				
KW	Signal.				
FT	SIGNAL	1	23	POTENTIAL.	
SO	SEQUENCE	127 AA;	14491 MW;	B851IDC3407AB69B CRC64;	
Query Match		98.8%;	Score 569;	DB 13;	Length 127;
Best Local Similarity		99.0%;	Pred. No. 1.9e-58;		
Matches	103;	Conservative	0;	Mismatches	1;
				Indels	0;
				Gaps	0;
OY	1	ODWLTFQKKHLNTRDVCNIIIMSTNLFHCKDKNTFIYSRPEPVAKICKGIATSNVLT	60		
Db	24	ODWLTFQKKHLNTRDVCNINIMSTNLFHCKDKNTFIYSRPEPVAKICKGIATSNVLT	83		

Oy	61	SEFYISDCNVTSR	PKYKKLKSTNTFCYTCENQAPRVHFGVGH	104
Db	84	SEFYISDCNVTSR	PKYKKLKSTNTFCYTCENQAPRVHFGVGH	127
RESULT	2			
O9DFY6				
ID	O9DFY6	PRELIMINARY:	PRT:	129 AA.
AC	O9DFY6:			
DT	01-MAR-2001	(TREMBLrel. 16, Created)		
DT	01-OCT-2001	(TREMBLrel. 18, Last sequence update)		
DT	01-DEC-2001	(TREMBLrel. 19, last annotation update)		
DE	RC-RNASE4 RIBONUCLEASE PRECURSOR.			
OS	Rana catesbeiana (Bull frog).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Ranidae; Rana.			
NCBI_TaxID=8400;				
SEQUENCE FROM N.A.				
RC	TISSUE=LIVER:			
RC	MEDLINE=20512555; PubMed=11058105;			
RA	Liao Y.-D., Huang H.-C., Leu Y.-J., Wei C.-W., Tang P.-C., Wang S.-C.;			
RT	"Purification and cloning of cytotoxic ribonucleases from Rana			
RT	catesbeiana (bullfrog)."			
RL	Nucleic Acids Res. 28:4097-4104(2000).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=LIVER:			
RA	Liao Y.-D., Huang H.-C., Leu Y.-J., Wei C.-W., Tang P.-C., Wang S.-C.;			
RL	Submitted (AUG-2001) to the EMBL/Genbank/DBJ databases.			
DR	EMBL: AF242555; AAC31441.2; "			
DR	HSSP: P22069; IONC			
DR	InterPro: IPR001427; RNaseA.			
DR	Pfam: PF00074; RNaseA; 1.			
DR	ProDom: PD000535; RNaseA; 1.			
DR	SMART: SM00092; RNase_Pc; 1.			
DR	PROSITE: PS00127; RNASE_PANCREATIC; UNKNOWN_1.			
KW	Signal.			
FT	SIGNAL	1	23	POTENTIAL.
FT	CHAIN	24	129	RC-RNASE4 RIBONUCLEASE.
SO	SEQUENCE	129 AA;	14724 MW;	826A6282B10ABDA CRC64;
	Query Match	68.7%;	Score 395.5;	DB 13; Length 129;
	Best Local Similarity	66.7%;	Pred. No. 2.6e-38;	
	Matches 70; Conservative	16;	Mismatches 16;	Indels 1; Gaps 1.
Oy	1	ODMLTFQKKHLNTRDVCNIMSTNLFHCKDKNTFYISRPVNAICKGIATSKNVLT	60	
Db	24	ODMATEFKKKHLDTWDVDCNDLMPISLDFCKDKNFTYISLPQVNAICGVI	83	
Oy	61	SEFYISDCNVTSR-PCKYKKLKSTNTFCYTCENQAPRVHFGVGH	104	
Db	84	SEFYLAECNVKPRKPKYKKLKSSNRICIRCHELHPVHFGVIC	128	
RESULT	3			
O9DFY8				
ID	O9DFY8	PRELIMINARY:	PRT:	128 AA.
AC	O9DFY8:			
DT	01-MAR-2001	(TREMBLrel. 16, Created)		
DT	01-MAR-2001	(TREMBLrel. 16, Last sequence update)		
DT	01-DEC-2001	(TREMBLrel. 19, last annotation update)		
DE	RC-RNASE2 RIBONUCLEASE PRECURSOR.			
OS	Rana catesbeiana (Bull frog).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Ranidae; Rana.			
NCBI_TaxID=8400;				
SEQUENCE FROM N.A.				
RC	TISSUE=LIVER:			
RC	MEDLINE=20512555; PubMed=11058105;			

Query Match	Best Local Similarity	67.2%;	Score 387;	DB 13;	Length 128;
Matches 70;	Conservative 10;	Mismatches 24;	Indels 0;	Gaps 0;	
QY 1	QDMLTFQKKHLNTRDVCNIMSTNLFHCKDKNTFIYSRPEPKAIKGIIASKNVLT	60			
DB 24	QWETTFQKKHLNTRDVCNIMSTNLFHCKDKNTFIYSRPEPKAIKGIIASKNVLT	83			
QY 61	SEFYISDCNVTSRPCKYKIKKSTNFCYTCENQAPVHFGVGHGHC 104				
DB 84	DEFLYISDCNRIKLPCHYKIKKSSNTICITENKLPVHEVAVEEC 127				
RESULT 4					
Q9DFY7	PRELIMINARY:	PRT,	128 AA.		
AC Q9DFY7;					
DT 01-MAR-2001 (TREMBLrel. 16, Created)					
DT 01-OCT-2001 (TREMBLrel. 18, Last sequence update)					
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)					
DE RANA-ENSE3 RIBONUCLEASE PRECURSOR.					
OS Rana catesbeiana (Bull frog).					
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;					
CC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Rana.					
OX NCBI_TaxID=8400;					
RN [1]					
RP SEQUENCE FROM N.A.					
RC TISSUE=LIVER;					
RX MEDLINE=20513555; PubMed=11058105;					
RA Liao Y.-D., Huang H.-C., Leu Y.-J., Wei C.-W., Tang P.-C., Wang S.-C.;					
RT "Purification and cloning of cytotoxic ribonucleases from Rana					
RL catesbeiana (bullfrog)."					
RN Nucleic Acids Res. 28:4097-4104(2000).					
RL Nucleic Acids Res. 28:4097-4104(2000).					
DR EMBL; AF242554; AAC31440.2; -					
DR HSSP; P22069; 10NC.					
DR InterPro: IPR001427; RNaseA.					
DR Pfam: PF00074; RNaseA; 1.					
DR ProDom: PD000535; RNaseA; 1.					
DR SMART; SM00092; RNase_Pc; 1.					
DR PROSITE; PS00127; RNASE_PANCREATIC; UNKNOWN_1.					
KW Signal.					
FT SIGNAL	1	23	POTENTIAL.		
FT CHAIN	24	128	RC-RNASE2_RIBONUCLEASE.		
FT SEQUENCE	128 AA;	14839 MW;	989719CF52053ECC CRC64;		
QY 1	QDMLTFQKKHLNTRDVCNIMSTNLFHCKDKNTFIYSRPEPKAIKGIIASKNVLT	60			
DB 24	QWETTFQKKHLNTRDVCNIMSTNLFHCKDKNTFIYSRPEPKAIKGIIASKNVLT	83			
QY 61	SEFYISDCNVTSRPCKYKIKKSTNFCYTCENQAPVHFGVGHGHC 104				
DB 84	DEFLYISDCNRIKLPCHYKIKKSSNTICITENKLPVHEVAVEEC 127				
RESULT 4					
Q9DFY7	PRELIMINARY:	PRT,	128 AA.		
AC Q9DFY7;					
DT 01-MAR-2001 (TREMBLrel. 16, Created)					
DT 01-OCT-2001 (TREMBLrel. 18, Last sequence update)					
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)					
DE RANA-ENSE3 RIBONUCLEASE PRECURSOR.					
OS Rana catesbeiana (Bull frog).					
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;					
CC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Rana.					
OX NCBI_TaxID=8400;					
RN [1]					
RP SEQUENCE FROM N.A.					
RC TISSUE=LIVER;					
RX MEDLINE=20513555; PubMed=11058105;					
RA Liao Y.-D., Huang H.-C., Leu Y.-J., Wei C.-W., Tang P.-C., Wang S.-C.;					
RT "Purification and cloning of cytotoxic ribonucleases from Rana					
RL catesbeiana (bullfrog)."					
RN Nucleic Acids Res. 28:4097-4104(2000).					
RL Nucleic Acids Res. 28:4097-4104(2000).					
DR EMBL; AF242554; AAC31440.2; -					
DR HSSP; P22069; 10NC.					
DR InterPro: IPR001427; RNaseA.					
DR Pfam: PF00074; RNaseA; 1.					
DR ProDom: PD000535; RNaseA; 1.					
DR SMART; SM00092; RNase_Pc; 1.					
DR PROSITE; PS00127; RNASE_PANCREATIC; UNKNOWN_1.					
KW Signal.					
FT SIGNAL	1	23	POTENTIAL.		
FT CHAIN	24	128	RC-RNASE2_RIBONUCLEASE.		
FT SEQUENCE	128 AA;	14517 MW;	2B1496082E0587D CRC64;		
Query Match	Best Local Similarity	55.0%;	Score 317;	DB 13;	Length 128;
Matches 57;	Conservative 13;	Mismatches 34;	Indels 0;	Gaps 0;	

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Db      24 QDMETFOKKHLTDYTKKKCCVEMAKALFDCKKNTFTYALPGRYKALCKNIRDNTVLISR 83
QY      61 SEFYLSDCNVTSRPCKYKLLKSTNTFCVTCENAPVHFVGVGHC 104
Db      84 DAFLLPQCDRIKLPCYKILSSSTNTICTTCVNOLPIHFAGVGC 127

RESULT 5
Q9DFY5 PRELIMINARY; PRT; 128 AA.
AC Q9DFY5;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-OCT-2001 (TREMBLrel. 18, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE RC-RNASE6 RIBONUCLEASE PRECURSOR.
OS Rana catesbeiana (Bull frog).
OC Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Ranidae; Rana.
OX NCBI_TaxID=8400;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=LIVER;
RA MEDLINE=20512555; PubMed=11058105;
RA Liao Y.-D., Huang H.-C., Liao Y.-J., Wei C.-W., Tang P.-C., Wang S.-C.;
RT "Purification and cloning of cytotoxic ribonucleases from Rana
RT catesbeiana (bullfrog).";
RL Nucleic Acids Res. 28:4097-4104(2000).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=LIVER;
RA Liao Y.-D., Huang H.-C., Liao Y.-J., Wei C.-W., Tang P.-C., Wang S.-C.;
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF242556; ANG31442.2; -
DR HSSP: p22069; IONC.
DR InterPro: IPR001427; RNaseA.
DR Pfam: PF00074; RNaseA.1.
DR ProDom: PD000535; RNaseA.1.
DR SMART: SM00092; RNase_Pc.1.
DR PROSITE: PS00127; RNASE_PANCREATIC; UNKNOWN_1.
KW Signal.
FT SIGNAL. 1 23 POTENTIAL.
FT CHAIN 24 128 RC-RNASE6 RIBONUCLEASE.
SQ SEQUENCE 128 AA; 14804 MW; AFEBF67D266C7C2 CRC64;

Query Match 54.7%; Score 315; DB 13; Length 128;
Best Local Similarity 53.8%; Pred. No. 5.7e-29;
Matches 56; Conservative 14; Mismatches 34; Indels 0; Gaps 0;

QY 1 QDWLTFQKKHLTNRDVCNITMSTNLFHCKDKNTFTYSRPEPYKATCKGIASKNVLTT 60
Db 24 QDMETFOKKHLTDYTKKKCCVEMAKALFDCKKNTFTYALPGRYKALCKNIRDNTVLISR 83
QY 61 SEFYLSDCNVTSRPCKYKLLKSTNTFCVTCENAPVHFVGVGHC 104
Db 84 DAFLLPQCDRIKLPCYKILSSSTNTICTTCVNOLPIHFAGVGC 127

RESULT 6
Q98SMO PRELIMINARY; PRT; 133 AA.
AC Q98SMO;
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE RNase A-TYPE RIBONUCLEASE RC208 PRECURSOR.
OS Rana catesbeiana (Bull frog).
OC Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Ranidae; Rana.
OX NCBI_TaxID=8400;
RN [1]
RP SEQUENCE FROM N.A.

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RX MEDLINE=21539506; PubMed=11683320;
RA Rosenberg H.F., Zhang J., Liao Y.-D., Dyer K.D.;
RT "Rapid diversification of RNase A superfamily ribonuclease from the
RT bullfrog, Rana catesbeiana.";
RL J. Mol. Evol. 53:31-38(2001).
DR EMBL: AF351209; AAK30255.1; -
DR HSSP: P11916; IBC4.
DR InterPro: IPR001427; RNaseA.
DR Pfam: PF00074; RNaseA.1.
DR ProDom: PD000535; RNaseA.1.
DR SMART: SM00092; RNase_Pc.1.
DR PROSITE: PS00127; RNASE_PANCREATIC; UNKNOWN_1.
KW Signal.
FT SIGNAL. 1 22 POTENTIAL.
SQ SEQUENCE 133 AA; 14628 MW; 87FC122C3499E02 CRC64;

Query Match 51.6%; Score 297; DB 13; Length 133;
Best Local Similarity 49.5%; Pred. No. 7.3e-27;
Matches 55; Conservative 16; Mismatches 32; Indels 8; Gaps 3;

QY 1 QDWLTFQKKHLTNRDVCNITMSTNLFHCKDKNTFTYSRPEPYKATCKGIASKN 56
Db 23 QNMAATFOKKHITNTSSINCNTIMDNNTIYVGQCKGVATFTISSATVKAICTGVI-NMN 81
QY 57 VLTTSSEFYLSDC--NVTSRPCKYKLLKSTNTFCVTCENAPVHFVGVGHC 104
Db 82 VLTSTRQNLNCTRTSTTPRCPYSRTENNITCVKCNQIPVHFAGIGRC 132

RESULT 7
Q9PWR7 PRELIMINARY; PRT; 133 AA.
AC Q9PWR7;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE RIBONUCLEASE PRECURSOR.
GN RCR.
OS Rana catesbeiana (Bull frog).
OC Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Ranidae; Rana.
OX NCBI_TaxID=8400;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=LIVER;
RX MEDLINE=98165825; PubMed=9497370;
RA Huang H.-C., Wang S.-C., Liao Y.-J., Lu S.-C., Liao Y.-D.;
RT "The Rana catesbeiana rcr gene encoding a cytotoxic ribonuclease.
RT Tissue distribution, cloning, purification, cytotoxicity, and active
RT residues for RNase activity.";
RL J. Biol. Chem. 273:6395-6401(1998).
DR EMBL: AF039104; AADI0702.1; -
DR HSSP: P11916; IBC4.
DR InterPro: IPR001427; RNaseA.
DR Pfam: PF00074; RNaseA.1.
DR ProDom: PD000535; RNaseA.1.
DR SMART: SM00092; RNase_Pc.1.
DR PROSITE: PS00127; RNASE_PANCREATIC; UNKNOWN_1.
KW Signal.
FT SIGNAL. 1 22 POTENTIAL.
FT CHAIN 23 133 RIBONUCLEASE.
SQ SEQUENCE 133 AA; 14762 MW; A7D62594F7D16F0C CRC64;

Query Match 50.5%; Score 291; DB 13; Length 133;
Best Local Similarity 49.5%; Pred. No. 3.6e-26;
Matches 55; Conservative 16; Mismatches 32; Indels 8; Gaps 3;

QY 1 QDWLTFQKKHLTNRDVCNITMSTNLFHCKDKNTFTYSRPEPYKATCKGIASKN 56
Db 23 QNMAATFOKKHITNTSSINCNTIMDNNTIYVGQCKGVATFTISSATVKAICTGVI-NMN 81

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OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Ranidae; Rana.  
OX NCBI\_TaxID=8400;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=LIVER;  
RX MEDLINE=20512555; PubMed=11058105;  
RA Liao Y.-D., Huang H.-C., Liao Y.-J., Wei C.-W., Tang P.-C., Wang S.-C.;  
RT "Purification and cloning of cytotoxic ribonucleases from Rana  
catesbeiana (bullfrog).";  
RL Nucleic Acids Res. 28:4097-4104(2000).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC TISSUE=LIVER;  
RA Liao Y.-D., Huang H.-C., Liao Y.-J., Wei C.-W., Tang P.-C., Wang S.-C.;  
RL Submitted (AUG-2001) to the EMBL/Genbank/DBJ databases.  
DR EMBL: AF288642; AAG30414.2; -.  
DR HSSP: P11916; 1BC4.  
DR InterPro: IPR001427; RNaseA.  
DR Pfam: PF00074; rnaaseA; 1.  
DR ProDom: PD000535; RNaseA; 1.  
DR SMART: SM00092; RNaseA; 1.  
DR PROSITE: PS00127; RNASE\_PANCREATIC; UNKNOWN\_1.  
KM Signal.  
FT SIGNAL 1 21 POTENTIAL.  
FT CHAIN 22 132 RC-RNASEL1 RIBONUCLEASE.  
FT SIGNAL 22 132 RC-RNASEL1 RIBONUCLEASE.  
SQ SEQUENCE 132 AA; 14625 MW; D8D9A517452FBE53 CRC64;

Query Match 47.7%; Score 274.5; DB 13; Length 132;  
Best Local Similarity 44.1%; Pred. No. 3e-24;  
Matches 49; Conservative 19; Mismatches 36; Indels 7; Gaps 2;

QY 1 ODWLTFQKKHLNTRDVCNIIIMSTNLF---HCKDKNTFIYSRPEPYKAIKGIISKVN 56  
DB 22 QNMATFQKHHTSTSSIDCNTMTKATITVGGCKEKERNFTISSDNNKAIKCSGVSPDK 81

QY 57 VLTSEFYLSDC---VTSRPCKYKLLKSTNFCVTCENQAPVHFVGVGHC 104  
DB 82 ELSTSFILNCTIRDSITPRPCVPHSPDNKNKICVCKEQLPVHRTVGIGKC 132

RESULT 12  
098SL8 PRELIMINARY; PRT; 133 AA.  
AC 098SL8:  
DT 01-JUN-2001 (TREMBLrel. 17, Created)  
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)  
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
DE RNase A-TYPE RIBONUCLEASE RC218 PRECURSOR.  
OS Rana catesbeiana (Bull frog).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Ranidae; Rana.  
OX NCBI\_TaxID=8400;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=21539506; PubMed=11683320;  
RA Rosenberg H.F., Zhang J., Liao Y.-D., Dyer K.D.;  
RT "Rapid diversification of RNase A superfamily ribonuclease from the  
bullfrog, Rana catesbeiana.";  
RL J. Mol. Evol. 53:31-38(2001).  
DR EMBL: AF351211; AAK30257.1; -.  
DR HSSP: P11916; 1BC4.  
DR InterPro: IPR001427; RNaseA.  
DR Pfam: PF00074; rnaaseA; 1.  
DR ProDom: PD000535; RNaseA; 1.  
DR SMART: SM00092; RNaseA; 1.  
DR PROSITE: PS00127; RNASE\_PANCREATIC; UNKNOWN\_1.  
KM Signal.  
FT SIGNAL 1 22 POTENTIAL.  
SQ SEQUENCE 133 AA; 14590 MW; 8B40B9A94FA5B943 CRC64;

Query Match 47.4%; Score 273; DB 13; Length 133;  
Best Local Similarity 45.9%; Pred. No. 4.5e-24;  
Matches 51; Conservative 18; Mismatches 34; Indels 8; Gaps 3;

QY 1 ODWLTFQKKHLNTRDVCNIIIMSTNLF---HCKDKNTFIYSRPEPYKAIKGIISKVN 56  
DB 23 QNMATFQKHHTSTSSIDCNTMTKATITVGGCKEKERNFTISSDNNKAIKCSGVSPDK 81

QY 57 VLTSEFYLSDC---VTSRPCKYKLLKSTNFCVTCENQAPVHFVGVGHC 104  
DB 82 VLSTKFDLDICTRIFTIPRCPYSSRIETNITCVKCNQIPVHFAGIGCC 132

RESULT 13  
09W738 PRELIMINARY; PRT; 169 AA.  
AC 09W738:  
DT 01-NOV-1999 (TREMBLrel. 12, Created)  
DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)  
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)  
DE FRU2 PROTEIN.  
OS Xenopus laevis (African clawed frog).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;  
OC Xenopodinae; Xenopus.  
OX NCBI\_TaxID=8355;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=96069863; PubMed=7589565;  
RA Kinoshita N., Minshall J., Kirschner M.W.;  
RT "The identification of two novel ligands of the fgr receptor by a  
yeast screening method and their activity in Xenopus development.";  
RL Cell 83:621-630(1995).  
RN [2]  
RP SEQUENCE FROM N.A.  
RA Kinoshita N., Kirschner M.W.;  
RL Submitted (JUN-1999) to the EMBL/Genbank/DBJ databases.  
DR EMBL: AF159166; AAD41901.1; -.  
DR HSSP: P00656; 1ISO.  
DR InterPro: IPR001427; RNaseA.  
DR Pfam: PF00074; rnaaseA; 1.  
DR ProDom: PD000535; RNaseA; 1.  
DR SMART: SM00092; RNaseA; 1.  
DR PROSITE: PS00127; RNASE\_PANCREATIC; UNKNOWN\_1.  
SQ SEQUENCE 169 AA; 18891 MW; D969F3E4B3CE1B8 CRC64;

Query Match 26.6%; Score 153.5; DB 13; Length 169;  
Best Local Similarity 35.8%; Pred. No. 4.3e-10;  
Matches 38; Conservative 20; Mismatches 37; Indels 11; Gaps 6;

QY 6 FQKKHLNTRDVCNIIIMSTNLF---HCKDKNTFIYSRPEPYKAIKGIISKVN 59  
DB 33 FMEKHIVKGAETNCNQTIKDRNIRFKNNCKERNFTIHDNCKKYEKAGIKSTFVIS 92

QY 60 TSEFYLSDC---TSRP--CKYKLLKSTNFCVTCENQAPVHFVGVGHC 100  
DB 93 KELPLUTDLIMGRTPARPCAYNOTRTTGYINITICENYFVHFAG 138

RESULT 14  
09UK15 PRELIMINARY; PRT; 152 AA.  
AC 09UK15:  
DT 01-OCT-2000 (TREMBLrel. 15, Created)  
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)  
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
DE EOSTINOPHIL-ASSOCIATED RIBONUCLEASE 10.  
GN EAR10.  
OS Mus saxicola (Spiny mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

